

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 2.

EXAMPLE 5

Construction of an over-expression vector with a fruit enhanced promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 3.

EXAMPLE 6

Generation of transformed Musa plants

Transformed Musa plants containing the vectors are produced by the method described in Sagi et al. (1995) Biotechnology. Vol. 13 pp 481-485. Regenerated transformed plants are identified by their ability to grow on hygromycin and grown to maturity. Ripening fruit are analysed for a modulation in their ripening related or senescence characteristics.

Other suitable transformation methods for banana are described in Sagi et al. (1994) Plant Cell Reports. Vol. 13. pp 262-266. and May et al. (1995) Biotechnology. Vol. 13 pp 486-492.

TABLE 1

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-1	Pulp Upregulated	U-U9	1	Isoflavone Reductase	61.6	714	Potato (<i>Solanum tuberosum</i>), X92075
SEQ-ID-NO-2	Pulp Upregulated	U-U17	1	Isoflavone Reductase	62.9	770	Potato (<i>Solanum tuberosum</i>), X92075
SEQ-ID-NO-3	Pulp Upregulated	U-U66	1.1	Isoflavonoid Reductase	60.0	722	<i>Arabidopsis thaliana</i> , Z49777
SEQ-ID-NO-4	Pulp Upregulated	U-U104	1	Isoflavonoid Reductase	60.6	696	<i>Arabidopsis thaliana</i> Z49777
SEQ-ID-NO-5	Pulp Upregulated	U-U13	1.1	Beta-1,3-Glucanase	58.5	585	Soybean (<i>Glycine max</i>), A26451
SEQ-ID-NO-6	Pulp Upregulated	U-U136	1.3	Beta-1,3-Glucanase	59.8	800	Barley (<i>Hordeum vulgare</i>), M91814
SEQ-ID-NO-7	Pulp Upregulated	U-U21	1.8	Transcriptional Activator	54.3	311	<i>Zea mays</i> , L13454

00/6/11
P262d

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-8	Pulp Upregulated	U-U31	0.55	S-adenosylhomocysteine Hydrolase	67.0	467	Orchid (<i>Phalaenopsis</i> sp.), X79905
SEQ-ID-NO-9	Pulp Upregulated	U-U131	1.8	S-adenosyl L-homocysteine Hydrolase	79.8	699	Wheat (<i>Triticum aestivum</i>), L11872
SEQ-ID-NO-10	Pulp Upregulated	U-U32	0.8	Beta-amylase	54.7	854	<i>Zea mays</i> , Z25871
SEQ-ID-NO-11	Pulp Upregulated	U-U55	0.8	O-methyl transferases	60.1	223	<i>Zea mays</i> , L14063
SEQ-ID-NO-12	Pulp Upregulated	U-U72	0.8	O-methyl transferase	60.6	226	<i>Zea mays</i> , L14063
SEQ-ID-NO-13	Pulp Upregulated	U-U68	1.8	Pectate Lyase	57.9	394	<i>Lilium longiflorum</i> , Z17328
SEQ-ID-NO-14	Pulp Upregulated	U-U69	1.7	Pectate Lyase	66.1	516	<i>Zea mays</i> , L20140
SEQ-ID-NO-15	Pulp Upregulated	U-U84	1.1	Pectate Lyase	65.8	736	<i>Lycopersicon esculentum</i> , X55193
SEQ-ID-NO-16	Pulp Upregulated	U-U89	1.6	Pectate Lyase	54.8	354	<i>Nicotiana tabacum</i> , X67158